AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1-65. (canceled).

66. (currently amended) An isolated or ~~first~~ purified first polypeptide which binds to a second polypeptide comprising SEQ ID NO:4, said first polypeptide comprising amino acids 380 to 599 of SEQ ID NO: 2, wherein said amino acids 380 to 599 are at the carboxy terminus of said first polypeptide.

67-71. (canceled).

72. (currently amended) An ~~A composition comprising a first~~ isolated or purified first polypeptide which binds to a second polypeptide comprising SEQ ID NO:4, ~~and a second isolated or purified polypeptide, wherein said first polypeptide and said second polypeptide specifically bind each other, wherein~~ said first polypeptide comprising the peptide of ~~comprises amino acids 1 to 39 of~~ SEQ ID NO: 6, wherein said peptide of SEQ ID NO:6 is ~~amino acids 1 to 39 are~~ at the carboxy terminus of said first polypeptide~~, and wherein said second polypeptide comprises SEQ ID NO:4~~.

73-87. (canceled).

88. (previously presented) An isolated or purified polypeptide consisting of the amino acid sequence of SEQ ID NO: 2.

89-90. (canceled).

91. (currently amended) An isolated or purified polypeptide ~~primase~~ which binds a polypeptide comprising SEQ ID NO:4, wherein said isolated or purified polypeptide ~~primase~~ comprises an amino acid sequence selected from the group consisting of:

(a) a first amino acid sequence having at least 95% identity to amino acids 1-599 of SEQ ID NO: 2~~, wherein amino acids of said first amino acid sequence corresponding to amino acids 561-599 of SEQ ID NO:2 have 100% identity with amino acids 561-599 of SEQ ID NO:2~~;

~~(b) a second amino acid sequence having at least 97% similarity to amino acids 1-599 of SEQ ID NO: 2, wherein amino acids of said second amino acid sequence corresponding to amino acids 561-599 of SEQ ID NO:2 have 100% identity with amino acids 561-599 of SEQ ID NO:2~~; and

(b~~e~~) a second ~~an~~ amino acid sequence comprising amino acids 1-599 of ~~set forth in~~ SEQ ID NO: 2; and wherein said isolated or purified polypeptide has ~~primase further possesses a biological activity selected from the group consisting of activation of DNA polymerase activity,~~ RNA primase activity~~, stimulation of helicase activity of *S. aureus* DnaC helicase, and stimulation of ATPase activity of *S. aureus* DnaC helicase~~.

92-104. (canceled).

105. (previously presented) An isolated or purified polypeptide comprising the amino acid sequence of SEQ ID NO: 2.

106. (previously presented) An isolated or purified fragment of *Staphylococcus aureus* DnaG primase set forth in SEQ ID NO: 2, wherein said fragment binds a polypeptide comprising SEQ ID NO:4, and wherein said fragment is selected from the group consisting of amino acids 229 to 599 of SEQ ID NO:2 and amino acids 380 to 599 of SEQ ID NO:2.

107-108. (canceled).

109. (new) A method for determining whether a candidate compound is an inhibitor of the polypeptide set forth in SEQ ID NO:2, comprising:

(a) contacting a polypeptide of any one of claims 88, 105 and 106 with a candidate compound,

(b) assaying for RNA primase activity of the polypeptide of (a), and

(c) comparing the results from the assay of (b) with results of an assay performed using a polypeptide identical to the polypeptide of (a) that has not been contacted with the candidate compound, wherein when the RNA primase activity of the polypeptide of (a) is decreased in the presence of the candidate compound compared to in the absence of the candidate compound, the candidate compound is determined to be an inhibitor of the polypeptide set forth in SEQ ID NO:2.

110. (new) A method for determining whether a candidate compound is an activator of the polypeptide set forth in SEQ ID NO:2, comprising:

(a) contacting a polypeptide of any one of claims 88, 105 and 106 with a candidate compound,

(b) assaying for RNA primase activity of the polypeptide of (a), and

(c) comparing the results from the assay of (b) with results of an assay performed using a polypeptide identical to the polypeptide of (a) that has not been contacted with the candidate compound, wherein when the RNA primase activity of the polypeptide of (a) is increased in the presence of the candidate compound compared to in the absence of the candidate

compound, the candidate compound is determined to be an activator of the polypeptide set forth in SEQ ID NO:2.

111. (new) A method for determining whether a candidate compound binds the polypeptide set forth in SEQ ID NO:2, comprising:

(a) contacting a polypeptide of any one of claims 88, 105 and 106 with a candidate compound,

(b) detecting binding of said candidate compound to the polypeptide of (a).

112. (new) A method for determining whether a candidate compound binds the polypeptide set forth in SEQ ID NO:2, comprising:

(a) contacting a cell expressing a polypeptide of any one of claims 88, 105 and 106 with a candidate compound,

(b) detecting binding of said candidate compound to the polypeptide of (a).

113. (new) The method of claim 111, further comprising measuring the ability of the candidate compound to increase or decrease the RNA primase activity of the polypeptide set forth in SEQ ID NO:2.

114. (new) The method of claim 112, further comprising measuring the ability of the candidate compound to increase or decrease the RNA primase activity of the polypeptide set forth in SEQ ID NO:2.

115. (new) The method of claim 111, wherein detection of said binding is performed by a technique selected from the group consisting of phage display, surface plasmon resonance, fluorescence resonance energy transfer, fluorescence polarization, scintillation proximity assay, biosensor assay, yeast two hybrid system, and affinity chromatography.

116. (new) The method of claim 112, wherein detection of said binding is performed by a technique selected from the group consisting of phage display, surface plasmon resonance, fluorescence resonance energy transfer, fluorescence polarization, scintillation proximity assay, biosensor assay, yeast two hybrid system, and affinity chromatography.

117. (new) The method of claim 109, wherein said candidate compound is selected from the group consisting of a small organic molecule, a peptide, a polypeptide and an antibody.

118. (new) The method of claim 110, wherein said candidate compound is selected from the group consisting of a small organic molecule, a peptide, a polypeptide and an antibody.

119. (new) The method of claim 111, wherein said candidate compound is selected from the group consisting of a small organic molecule, a peptide, a polypeptide and an antibody.

120. (new) The method of claim 112, wherein said candidate compound is selected from the group consisting of a small organic molecule, a peptide, a polypeptide and an antibody.